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GenCore version 5.1.6
(c) 1993 - 2003 Compu

protein search, using sw model

June 9, 2003, 06:27:29 ; Search time 17 Seconds
(without alignments)

919.799 Million cell updates/sec

US-10-091-628-2
1979

BLOSUM62 Case 0

112892 segs, 41476328 residues

hits satisfying chosen parameters:

length: 20000000000

Minimum	Match	0%
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Listing first 45 summaries

SwissProt_40:*

is the number of results predicted by chance to have a value greater than or equal to the score of the result being printed derived by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
44.8	347	1	NTCI_RABIT	Q28727 o ileal soc
44.7	348	1	NTCI_CRIBR	Q60414 c ileal soc
44.0	348	1	NTCI_PAT	Q62623 r ileal soc
43.5	348	1	NTCI_HUMAN	Q12968 h ileal soc
28.3	362	1	NTCP_RAT	P26435 ratus norv
27.9	349	1	NTCP_HUMAN	Q14973 homo sapien
27.9	362	1	NTCP_MOUSE	Q08705 mus musculu
16.9	477	1	P3_HUMAN	P09131 homo sapien
9.1	182	1	P3_MOUSE	P12129 mus musculu
6.3	421	1	YCCA_BACCU	Q08791 bacillus stu
5.9	721	1	YUJY_ECOLI	P29366 escherichia
5.8	286	1	YCKE_BACME	P40419 bacillus me
5.7	368	1	Y944_SYNT3	P43310 anophel
5.5	383	1	Y544_SYNT3	P33510 anophel
5.4	576	1	N55M_ANOOU	P34310 anophel
5.4	443	1	COXX_HUMAN	Q12887 homo sapien
5.3	397	1	YGED_ECOLI	P31916 escherichia
5.3	551	1	LLDP_ECOS7	Q8Xdf9 escherichia
5.3	551	1	LLDP_ECOLI	P33231 escherichia
5.1	532	1	YCI18_HAEIN	Q57221 haemophilu
5.0	332	1	YFPH_ECOLI	P39836 escherichia
5.0	379	1	CVB_BOLAM	P11722 bolovys am
5.0	387	1	GALS_HUMAN	Q43603 homo sapien
5.0	436	1	SECY_METTA	Q60175 methanococ
5.0	541	1	NDEM_ARTRF	Q37710 artemia sal
5.0	512	1	CCSA_ODOSI	P49523 odontella s
5.0	333	1	YK26_PSEAE	P39879 pseudomonas
5.0	391	1	SOTB_HELPJ	Q9ZK31 helicobacte
5.0	391	1	YIDY_ECOLI	P31462 escherichia
5.0	835	1	CD97_HUMAN	P48960 homo sapien
4.9	460	1	YUJY_ECOLI	P31435 escherichia
4.9	369	1	MRAY_ANASAP	Q0ypk3 anabena sp

ALIGNMENTS

ID	NCBI_RABIT	STANDARD;	PRT;	347 AA.
AC	028727;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Ileal sodium/bile acid cotransporter (Ileal Na(+)/bile acid cotransporter) (Na+ dependent ileal bile acid transporter) (Ileal sodium-dependent bile acid transporter) (ISBT) (Sodium/taurocholate cotransporting polypeptide, ileal).			
GN	SUC10A2 OR NTC2P.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxId=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=New Zealand white; TISSUE=Illum;			
RA	Stengelin S., Apel S., Becker W., Maier M., Rosenberger J., Wess G., Kramer W.;			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: PLAYS A CRITICAL ROLE IN THE SODIUM-DEPENDENT TRANSPORT OF BILE ACIDS FROM THE LUMEN OF THE SMALL INTESTINE.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE SODIUM:BILE ACID SYMPORTER FAMILY (SBF).			
CC	-----			
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CC				
DR	EMBL; Z54357; CAA91184.1; -			
DR	EMBL; AJ002005; CAA05135.1; -			
DR	InterPro; IPR004710; Bass.			
DR	InterPro; IPR002657; BileAc/Na_smprtr.			
DR	Pfam; PF01756; SBF; 1.			
DR	TIGRFAMs; TIGR00841; Bass; 1.			
KW	Transmembrane; Transport; Symport; Sodium transporter; Glycoprotein.			
FT	TRANSMEM 30 50 POTENTIAL.			
FT	TRANSMEM 59 79 POTENTIAL.			
FT	TRANSMEM 83 103 POTENTIAL.			
FT	TRANSMEM 128 148 POTENTIAL.			
FT	TRANSMEM 159 179 POTENTIAL.			
FT	TRANSMEM 197 217 POTENTIAL.			
FT	TRANSMEM 226 246 POTENTIAL.			
FT	TRANSMEM 290 310 POTENTIAL.			
FT	CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).			
SO	SEQUENCE 347 AA; 37729 MW; 1315B6BADDE66C CRC64;			

Query Match 44.8%; Score 886; DB 1; Length 347;

FT TAUCHOLATE TRANSPORT.
 FT /FTid=VAR_004615.
 FT P -> S (IN CD; ABOLISHES TAUCHOLATE
 FT TRANSPORT).
 FT /FTid=VAR_004616.
 SQ SEQUENCE 348 AA; 34897 MM; 159900AAA91CCD06 CRC64;
 Query Match 43.5%; Score 860.5; DB 1; Length 348;
 Best Local Similarity 45.6%; Pred. No. 2.7e-49;
 Matches 160; Conservative 58; Mismatches 104; Indels 19; Gaps 4;

QY 5 CSSSSACPRASSEELPVGLEVHGNLEIVTVSTVMGMLMSLGCSEVIRLMSHIR 64
 DB 14 CCGACVCPBSNNNI-----LSVSLVTLTLALVWFSWCGNVEIKFELCHIRK 64
 QY 65 PMGIAGVLLCOFGLMFTAYLLAISFLKPVQAVLIMCCPGGTISNIFTEWVDGMD 124
 DB 65 PMGICVGLCOFGLMFTAYLLAISFLKPVQAVLIMCCPGGTISNIFTEWVDGMD 124
 QY 125 LSIISMTGCTVAALGMPPLCIYITWSMSLQONLTPYQNIITLVCLTIPVAFGVYVNY 184
 DB 125 LSIISMTGCTVAALGMPPLCIYITWSMSLQONLTPYQNIITLVCLTIPVAFGVYVNY 184
 QY 185 RMPKSKIIILKIGAVVGVLLVAVAGVVLAKGSNNSDITLITISFIPILGHVTFGL 244
 DB 185 RMPKSKIIILKIGAVVGVLLVAVAGVVLAKGSNNSDITLITISFIPILGHVTFGL 244
 QY 245 ALFTHSQMCRRTISLETGQNIQMCITMQLSFTAEHLVOMLSPFLAYGLFQILDGFLI 304
 DB 245 ALFTHSQMCRRTISLETGQNIQMCITMQLSFTAEHLVOMLSPFLAYGLFQILDGFLI 304
 QY 305 VAAVQYKRLKRNKHKKSGCTEVCHTRKSTSSRETNAFLEVNEGAIPT 355
 DB 305 VAAVQYKRLKRNKHKKSGCTEVCHTRKSTSSRETNAFLEVNEGAIPT 355
 QY 305 LGFYVAYKK-----CHGKNKAEIPE-----SKENGTBESSFYKKN--CGFOP 345
 DB 305 LGFYVAYKK-----CHGKNKAEIPE-----SKENGTBESSFYKKN--CGFOP 345

RESULT 5
 NTCIP_RAT STANDARD; PRT; 362 AA.
 ID NTCIP_RAT STANDARD; PRT; 362 AA.
 AC P26435;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Sodium/bile acid cotransporter (Na(+)/bile acid cotransporter)
 DE (Na(+)/taurocholate cotransport protein) (Sodium/taurocholate cotransporting polypeptide).
 DE SLC10A1 OR NTCIP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92073340; PubMed=1961729;
 HA Hagenbuch B., Stieger B., Foguet M., Luebert H., Meier P.J.; Functional expression, cloning and characterization of the hepatocyte Na(+)/bile acid cotransporter system; J Biol Chem 268:10629-10633 (1991).
 CC Proc. Natl. Acad. Sci. U.S.A. 88:10629-10633 (1991).
 CC FUNCTION: THE HEPATIC SODIUM/BILE ACID UPTAKE SYSTEM EXHIBITS BROAD SUBSTRATE SPECIFICITY & TRANSPORTS VARIOUS NONBILE ACID ORGANIC COMPOUNDS AS WELL. IT IS STRICTLY DEPENDENT ON THE EXTRACELLULAR PRESENCE OF SODIUM.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC TISSUE SPECIFICITY: LIVER AND KIDNEY.
 CC SIMILARITY: BELONGS TO THE SODIUM/BILE ACID SYMPORTER FAMILY. (SBR).
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 CC EMBL; M77479; AAA42112.1; -
 CC DR PIR; A41601; A41601.
 CC DR InterPro; IPR004710; Baaa.
 CC DR InterPro; IPR002657; BileAc/Na_smptr.
 CC DR Pfam; PF01758; SBR; 1.
 CC DR TIGR; PIR; TIGR00841; Baaa; 1.
 CC TRASNEMEMbrane; Transport; Symport; Sodium transport; Glycoprotein.
 FT TRASNEMEM 24 45
 FT TRASNEMEM 60 80
 FT TRASNEMEM 82 98
 FT TRASNEMEM 158 178
 FT TRASNEMEM 190 211
 FT TRASNEMEM 228 244
 FT TRASNEMEM 285 306
 FT CARBOHYD 5 5
 FT CARBOHYD 11 11
 FT CARBOHYD 103 103
 FT CARBOHYD 117 117
 FT CARBOHYD 271 271
 SQ SEQUENCE 362 AA; 36245 MM; FOAB376076A57550 CRC64;
 Query Match 28.3%; Score 559.5; DB 1; Length 362;
 Best Local Similarity 37.2%; Pred. No. 9.7e-30;
 Matches 133; Conservative 69; Mismatches 135; Indels 21; Gaps 9;

QY 10 ACPANSEEDLPGVLEHGNLEIVTVSTVMGMLMSLGCSEVIRLMSHIRPWCIA 69
 DB 7 SAPNFS---LPRGCG-HRADKALSIIVLMLIMLSLGTWFSKIKALMKPKVVI 62
 QY 70 VGLLQFGLMFTAYLLAISFLKPVQAVLIMCCPGGTISNIFTEWVDGMDLISGM 129
 DB 63 VALVAGFQIMPLAALGKIFHLSNIEALADICGSPGMSINFTLAMKGMMLISYM 122
 QY 130 TTCSTVAALGMPPLCIYITWSMSLQONLTPYQNIITLVCLTIPVAFGVYVNY 186
 DB 123 TTCSTVAALGMPPLCIYITWSMSLQONLTPYQNIITLVCLTIPVAFGVYVNY 180
 QY 187 PKOSKIIILKIGAVVGVLLVAVAGVVLAKGSNNSDITLITISFIPILGHVTFGL 244
 DB 181 PHVYVYLKGMPLIIFLVSANVTALSVNGSINFWMTPHLANSLSMPSGFLMGYIL 240
 QY 245 -ALFTHSQMCRRTISLETGQNIQMCITMQLSFTAEHLVOMLSPFLAYGLFQILDGFLI 302
 DB 241 SALF--QINPSCRRRTISMETGFQNIQMCITMQLSFTAEHLVOMLSPFLAYGLI 298
 QY 303 LIVAAYQYKRLKRNKHKKSGCTEVCHTRKSTSSRETNAFLEVNEGAIPT 360
 DB 299 LIIIFRCYEKI-----KPPKDYKTYKKAATEDATPALEKGTTHNGNIPPLQGP 350

RESULT 6
 NTCIP_HUMAN STANDARD; PRT; 349 AA.
 ID NTCIP_HUMAN STANDARD; PRT; 349 AA.
 AC Q14973;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/bile acid cotransporter (Na(+)/bile acid cotransporter)
 DE (Na(+)/taurocholate cotransport protein) (Sodium/taurocholate cotransporting polypeptide).
 DE SLC10A1 OR NTCIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94179485; PubMed=8132774;
 HA Hagenbuch B., Meier P.J.;

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AC 0008705; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Sodium/bile acid cotransporter (Na(+)/bile acid cotransporter)
DE (Na(+)/taurocholate transporter protein) (Sodium/taurocholate
DE cotransporting polypeptide).
GN SLC10A1 OR NTCF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Saeki T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Hagedorn B.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE HEPATIC SODIUM/BILE ACID UPTAKE SYSTEM EXHIBITS
CC BROAD SUBSTRATE SPECIFICITY & TRANSPORTS VARIOUS NONBILE ACID
CC ORGANIC COMPOUNDS AS WELL. IT IS STRICTLY DEPENDENT ON THE
CC EXTRACELLULAR PRESENCE OF SODIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SODIUM/BILE ACID SYMPORTER FAMILY
CC (SBP).
CC -----
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CC -----
DR EMBL; AB003303; BAA19846.1; -.
DR EMBL; U95131; AAB81023.1; -.
DR MGI; 97379; Slc10a1.
DR InterPro; IPR004710; Base.
DR InterPro; IPR002657; BileAc/Na_smptr.
DR Pfam; PFO1758; SBF; 1.
DR TIGRFAMs; TIGR00841; base; 1.
KM Transmembrane; Symport; Sodium transporter; Glycoprotein.
FT FT 24 45
FT TRANSMEM 60 80
FT TRANSMEM 82 98
FT TRANSMEM 158 178
FT TRANSMEM 190 211
FT TRANSMEM 228 244
FT TRANSMEM 285 306
FT CARBOHYD 5 5
FT CARBOHYD 11 11
FT CARBOHYD 103 103
FT CARBOHYD 117 117
FT CARBOHYD 271 271
SQ SEQUENCE 362 AA; 39413 MW; 7A70493BE1804280F CXC64;
Query Match 27.9%; Score 553; DB 1; Length 362;
Best Local Similarity 35.1%; Pred. No. 2,6e-29;
Matches 129; Conservative 72; Mismatches 142; Indels 24; Gaps 8
QY 10 ACPANSESEELPVGLEVGHNLDELVTYVSTVMGILMFLSCSYEIRLMSHIRPAGIA 69
DB 7 SAPANS--LPPGFG-HRADTALSTVLIVWMLTLMISLDCCTMEFSKIAHFKVKGVI 62
QY 70 VGLICFGMLPFAVYLAIAISFSLKLVQVIAVLVLMGCCPGGTISNIFTFWVGDMDLSISM 129
DB 63 IAIYAQYGMPLSAIFLKGVPFLHTSEALAILICGCSGCVLSULFTIAMKGDNLSTIW 122
QY 130 TTCSTVAALGMPDLCTIYLT--MSMSLQDNLTIPYQNIIGITLVCLTIPVAFGYVANYRW 186

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Db      123 TTCSSTFALGMPPLLLYYTSKGIYDGLDKD--VPYKGMISLWVLLPCALIGIFLRSKR 180
QY      187 PRQSKIIILKIGAVVCGVLLLVAVAGVVLAKSNNSDIT--LLTISFIFPLIGHATGFL 244
Db      181 PHVYVYVAKAGMIIFFSLSVAATVLSVINGNSIMFYVTPHLLATSSLMFPGLMGYIL 240
QY      245 ALFTQSQRORCRSTISLETGAONICQIMTALQSFPAEHLVQMLSPFLAYGFPQLIDGFLI 304
Db      241 SALPFLNNSCRRTIMETGTFQVQVLCSTILANTPPEVIGLPFFPFLYIMFQALGELF 300
QY      305 VAAVQTYRRRLKNGKKGKKNCGCTEVQCHTRKSTSSRETNAPLEVNEEGAIITPGPPGDMCH 364
Db      301 IIFRCY---LKIKPKQKD---TKITTYAAATADATPAALEKGTINGNPNPTPG----- 349
QY      365 RALEPVG 371
Db      350 --LSPNG 354

RESULT 8
HUMAN
P3_HUMAN          STANDARD;          PRT;          477 AA.
P05331
01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P3 protein.
GN P3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP      SEQUENCE FROM N.A.
RX MEDLINE=89041548; PubMed=3186440;
RA "Alcalay M., Toniolo D.;
RT "CpG islands of the X chromosome are gene associated.";
RL Nucleic Acids Res. 16:9527-9556(1988).
[2]
RN RP      SEQUENCE FROM N.A.
RX MEDLINE=96311563; PubMed=8733135;
RA Chen E.Y., Zollo M., Mazarella R.A., Ciccodicola A., Chen C.-N.,
RA Zhu L., Heiner C., Burrough F.W., Ripetto M., Schlessinger D.,
RA D'Urso M.;
RT "Long-range sequence analysis in Xq28: thirteen known and six
RT candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
RT G6PD loci.";
RL Hum. Mol. Genet. 5:659-668(1996).
-1- FUNCTION: THE UBIQUITOUS EXPRESSION AND THE CONSERVATION OF THE
SEQUENCE IN DISTANT ANIMAL SPECIES SUGGEST THAT THE GENE CODES FOR
A PROTEIN WITH HOUSEKEEPING FUNCTIONS.
-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-1- SIMILARITY: TO P3 PROTEIN OF ANIMALS AND YEASTS.
-1- SIMILARITY: BELONGS TO THE SODIUM:BILE ACID SYMPORTER FAMILY
(SBP).
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CC -----
DR EMBL, X12458; CAA30998.1; -
DR EMBL, L44140; AAA92651.1; -
DR PIR, S01696; S01696.
DR MIM, 312090; -
DR InterPro, IPR004710; Baas.
DR InterPro, IPR002657; BileAc/Na_smptr.
DR Pfam, PF01758; SBP.1.
DR TIGRfams, TIGR00841; baas; 1.

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SQ      Transmembrane; Transport; Symport.
SQ      SEQUENCE 477 AA; 50332 MW; 49CB363EB3B66A1D CRC64;

Query Match 16.9%; Score 333.5; DB: 1; Length 477;
Best Local Similarity 31.5%; Pred. No. 5.8e-15;
Matches 87; Conservative 53; Mismatches 115; Indels 21; Gaps 3;

QY      12 PANSSEELPGLGVHGNLEIVFVTVVMGMLFSLGSGVEIRKLMSHRRPWIAGV 71
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      172 PAEDTPATLSADLHAFSENPFLVLLPLIFPKKSF--GCKVELEVLKGLMQSPQMLLG 229
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      72 LLQFGMLPFPAVYLLAISFSLKPAQVLAIVLMGCCPGGTSINITFWVDGMDISMTT 131
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      230 LLGQFLVWPLPAFLMAKVFMLPKALAGLIITCSSPGGGSYLSFLSLGQDVTLAISMTP 289
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      132 CSTVAALGMPPLCYLTLYWMSLSQONTIPYONIGITLVCTLIPAVGVVNYNMPKROSK 191
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      290 LSTVAAGFLPLSSAISIRLSLSHETLHVPISKLGLTLPLAIVANGVLKSLPFSQ 349
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      192 ILKIGAVGVGVL-----VVAAGVLIKAKSWSNDITLITSFIFPLIGHVTG 241
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      350 LLQVWVPFSPVLLLGFLFLAYRMGVFLAGIRL-----PIVAGIVPLVGLHVG 400
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      242 FLALFTHQSWQRCRTISLNGAONIOMCTIMLOLS 277
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      401 YCLATCKLPVQRRTVSIEVGONSLLALMIQLS 436
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
P3_MOUSE STANDARD; PRT; 182 AA.
ID P3_MOUSE
AC P21129;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, License annotation update)
DE P3 protein (Fragment).
GN P3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STAIN=BALE/C; TISSUE=Liver;
RX MEHLIN=90307023; Pubmed=1973144;
RA Filippi M., Tribioli C., Toniolo D.;
RT "Linkage and sequence conservation of the x-linked genes DKS235E (P3)
RT and DKS254E (Gdx) in mouse and man.";
RL Genomics 7:453-457(1990).
CC -1- FUNCTION: THE UBQUITOUS EXPRESSION AND THE CONSERVATION OF THE
CC SEQUENCE IN DIURNAL ANIMAL SPECIES SUGGEST THAT THE GENE CODES FOR
CC A PROTEIN WITH HOUSEKEEPING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE SODIUM:BILE ACID SYMPORTER FAMILY
CC (SBF).
CC -----
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CC -----
DB EMBL, J04761; AAA40519.1; -
DR InterPro, IPR002657; Billeac/Na_smprtr.
DR Pfam, PF01758; SBF, 1.
KM Transmembrane; Transport; Symport.
FT NON TER 1
SQ SEQUENCE 182 AA; 19629 MW; 472D732820CD620 CRC64;

Query Match 9.1%; Score 180.5; DB: 1; Length 182;
Best Local Similarity 30.2%; Pred. No. 2.1e-05;

```


Matches 45; Conservative 31; Mismatches 54; Indels 19; Gaps 2;

OY 139 GMPPLCYLWMSLQONLTPYONIGTLVCLTPAPFGYVYVYRMPKSKILKIGA 198
 DB 2 GFLPSSAIYSYLSIHETLHVPISKIGTLFLPIAAGVYVSKPKSEKELLQVTK 61

OY 199 VVGWGLT-----VVAVAVGLAKGSWNSDITLTLSIFPILIGHVTFLLAFT 248
 DB 62 PFSFLLGLFLAHMGVFLVGVRL-----PIVGVFTVPLVGLVGSIALCL 112

OY 249 HOSWORCFTISLETGAONIQMCITMLOLS 277
 DB 113 KLPVQORRTVSIEVGQNSLALAMLQLS 141

RESULT 10
 YCXA_BACSU STANDARD; PRT; 409 AA.
 Q06751;
 01-FEB-1995 (Rel. 31, Created)
 01-FEB-1995 (Rel. 31, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein ycxA (ORF5).
 GN YCXA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=93360813; PubMed=8355609;
 RA Cosmina P., Rodriguez F., de Ferra F., Grandi G., Pergo M.,
 RA Venema G., van Sinderen D.; the genetic locus responsible for surfactin
 RT synthesis and analysis of the genetic locus responsible for surfactin
 RL Mo1. Microbiol. 8:821-831(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124189; PubMed=8969502;
 RA Yamane K., Kumano M., Kurita K.;
 RT "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:
 RT determination of the sequence of a 146 kb segment and identification
 RT of 113 genes";
 RL Microbiology 142:3047-3056(1996).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96804403; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolecin A., Borchert S.,
 RA Bottari R., Boutsier L., Brans A., Braun M., Brignell S.C., Broh S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Ertter J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Guim S.Y., Glaser P., Goffeau A., Golightly E.D., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kasser-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsreid G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Nasuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetlelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rappoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan B., Schleich S., Schroeter R., Scofield S.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solido B.,
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takashimi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambert R., Wedler E., Wedler H., Weitzenecker T.,
 RA Wintere P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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 CC
 CC EMBL; X70356; CAA49820.1; -
 CC EMBL; D50453; BAA08987.1; -
 CC EMBL; Z99105; CAB12147.1; -
 CC EMBL; Z99106; CAB12161.1; -
 CC Subtilisin; BG10172; YCXA.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 9 29
 FT TRANSMEM 49 69 * POTENTIAL.
 FT TRANSMEM 77 97 POTENTIAL.
 FT TRANSMEM 100 120 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 217 237 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT TRANSMEM 284 304 POTENTIAL.
 FT TRANSMEM 309 329 POTENTIAL.
 FT TRANSMEM 341 361 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 SQ SEQUENCE 409 AA; 44858 MW; 8958A43B07E29D3 CRC64;

Query Match 6.3%; Score 125; DB 1; Length 409;
 Best Local Similarity 20.9%; Pred. No. 0.17;
 Matches 78; Conservative 61; Mismatches 122; Indels 112; Gaps 19;

OY 20 LPVGLHVGNGLEVTAVSTVM--GLMFLGCSV--IRKLSHRRMGIAVGLLC 74
 DB 34 LPMADAFHADRSLISVSISIMITGIVQFVGFIDRFVRKI-----MALGAVC 84

OY 75 --QGLMPTFAVLLAISFSLKPVQAIIVLNG-----CCPGATISNIFFWVDGMDLSI 127
 DB 85 ISASLVLPYPNNVHVS-----AIVGVLGIGYSCAVGTVQYFISCFDTHKGLAL 137

OY 128 SMTTGSYVALGMPPLCYL--YVWSLSLOONLTPYONIGTLVCLTP-VAFG---- 179
 DB 138 AILTVANSAGLVSPPIWAAAPYAGW--OSTVTI-----LGIWAAVLVPLVFGMKHP 191

OY 180 -----VYVAVRW-----PKOSKI--ILKIGAVGSLLVV-----AV 210
 DB 192 PHAQAEIVKSYDMRGFWNNMKOSKLIHLVGFVTCFTMGITDAHLVPLIKAHVSHV 251

OY 211 AGVVALAKS-----ANSDI-----TLTTSIFPILIGHVTFLLAFTHOS--W- 252
 DB 222 NGWMAAPAFPIIIGSLAGWISDLGSRVWLSIFIRLSLCLLPILIGIHSDLMY 311

OY 253 -----ORRTISLETGAONIQMCITMLOLSFPAHNVQMLSPPLAYG 294
 DB 312 FGFILLFGLSYTGVPLTPASISSEYQYG-----LIGSLIGNFPIHGVAGSLVYAGGL 366

OY 295 LFOIDGFLIYVA 307
 DB 367 FFDWTHGYLLIYA 379

RESULT 11

RESULT 13

OPRD_HUMAN STANDARD; PRT; 372 AA.

AC P41143; 01-FEB-1995 (Rel. 31, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Delta-type opioid receptor (DOR-1).

GN OPRD1 OR OPRD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_Taxid=9606;

[1]

RP SEQUENCE FROM N.A.

RP TISSUE=Brain cortex, and Striatum;

RP MEDLINE=94260835; PubMed=8201839;

RP Knapp R.J., Malatynska E., Fang L., Li X., Babin E., Nguyen M., Santoro G., Varga E.V., Hruby V.J., Roeseke W.R., Yamamura H.I.; "Identification of a human delta opioid receptor: cloning and expression.";

RP Life Sci. 54:PL463-PL469(1994).

[2]

RP SEQUENCE FROM N.A.

RP MEDLINE=95107267; PubMed=7808419;

RP Simoin F., Befort K., Gaveriaux-Ruff C., Matthes H., Nappay V., Lannes B., Micheletti G., Kleffer B.; "The human delta-opioid receptor: genomic organization, cDNA cloning, functional expression, and distribution in human brain.";

RP Mol. Pharmacol. 46:1015-1021(1994).

[3]

RP SEQUENCE FROM N.A.

RP Graham D.; Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

[4]

RP VARIANT PHE-27.

RP MEDLINE=20434920; PubMed=10982041;

RP Gelernter J., Kranzler H.R.; "Variant detection at the delta opioid receptor (OPRD1) locus and population genetics of a novel variant affecting protein sequence.";

RP Hum. Genet. 107:86-88(2000).

CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

CC EMBL; U07862; AAA18789.1; -

CC EMBL; U10504; AAA83426.1; -

CC EMBL; AL009181; CAAL5671.1; -

CC Genew; HGNC:8153; OPRD1.

CC MIM: 165195; -

CC InterPro; IPR000276; GPCR_Rhodopsn.

CC Pfam; PF00001; 7tm_1; 1.

CC PRINTS; PR00237; GPCR_RHODOPSIN.

CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.

CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate; Polymorphism.

CC DOMAIN 1 45

CC TRANSMEM 46 75

CC DOMAIN 76 84

CC CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 85 102

CC 2 (POTENTIAL).

FT DOMAIN 103 124

FT TRANSMEM 125 144

FT DOMAIN 145 174

FT TRANSMEM 175 190

FT DOMAIN 191 215

FT TRANSMEM 216 238

FT DOMAIN 239 261

FT TRANSMEM 262 284

FT DOMAIN 285 293

FT TRANSMEM 294 310

FT DOMAIN 311 372

FT CARBOHYD 18 18

FT CARBOHYD 33 33

FT DISULFID 121 198

FT LIPID 333 333

FT VARIANT 27 27

FT CONFLICT 40 41

FT CONFLICT 348 348

FT CONFLICT 370 370

FT SEQUENCE 372 AA; 40368 MW; 9D483FC93BA2BAE4 CRC64;

Query Match 5.8%; Score 114; DB 1; Length 372;

Best Local Similarity 21.3%; Pred. No. 0.81;

Matches 89; Conservative 61; Mismatches 150; Indels 118; Gaps 20;

QY 3 ANCSSS--SACPANSSSEELPVGLEHGNLELVTVSTVMGLMPSLGSEIRKLMS 60

DB 17 ANASDAYSACPSAGANASGPPGARSASLALAIATA--LVSACAV----- 62

QY 61 HIRPWGIAVLLCOFGLMPTAVLAIS--FSIKPQAVLAVLIMGCGPGTISNIPTF 117

DB 63 -----GLGNVLWFGIVRTYTKTKATNITYFNALADALATSTL--PQSAKYLME 113

QY 118 WVDGMDLSISMTSCSTVAALGMPLCIYLTWSMSLQOULTIPYONIGITVCLT--- 173

DB 114 WPFGL-----LCKAV-----LSIDYNNFTSIFLTWMSV 144

QY 174 ---IPVAGV-YVNYRMKSKII---LKIGAVGVLLVAVNA-----GVVLA-----K 217

DB 145 DRYIAVCHPVALDFRPPAKKLTINICWVASGVGVIMVAATRPDGVAVVCMLOPPS 204

QY 218 GSNMSD-----ITLLTISFIPFLIGHVTFGLALFTHSGMCRSTSETGAQNIQMC--- 270

DB 205 PSWMDVTKICVPLFAVVPILLITYCYGMLL-----RLKSVRLSSGKEKDRSLRR 258

QY 271 ITMLQSTFAELVQMSFPLAYGLFOLID-----GFLVAAYQYKRLKNKHKQNSGC 326

DB 259 ITRMVLVVVGAFFVCMAPRHFVLIWTLVIDRRDPLVVAL-----HLCIALGYANSSL 313

QY 327 TEVCHTRKSTSSRETNALVNEGCATP-----GPGPMDCRALEPVG--HTSC 376

DB 314 NPVLV-----AFLDENFKRCFRLCKRKGPDGPPSFSRAEATARERTVAC 360

RESULT 14

CYB_TOXGO STANDARD; PRT; 368 AA.

AC O20672; O20928; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Cytochrome B.

GN COB OR CYTB OR CYB.

OS Toxoplasma gondii.

OC Mitochondrion.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida; Sarcocystidae;

CC Toxoplasma.

CC NCBI_Taxid=5811;

CC [1]

CC SEQUENCE FROM N.A.

CC Touseil C., Tomavo S.; "Cytochrome B of Toxoplasma gondii.";

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 10-368 FROM N.A.
 RC STRAIN=RH;
 RA McFadden D.C., Boothroyd J.C.;
 RT "Cytochrome B gene from *Toxoplasma gondii*";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBIOINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS.
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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 CC
 DR EMBL; AF023246; AAC34138.1; -;
 DR InterPro; IPR000179; Cyt b b6.
 DR Pfam; PF00032; cytochrome b C; 1.
 DR Pfam; PF00033; cytochrome b N; 1.
 DR PROSITE; PS00192; CYTOCHROME B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME B_HEME; 1.
 DR Electon transport; Mitochondrion; Respiratory chain; Transmembrane;
 KW Heme.
 FT METAL 82 82 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 96 96 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 178 178 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 192 192 IRON 1 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 368 AA; 41594 MW; CCTG6B03784287CA CRC64;
 Query Match 5.7%; Score 112.5; DB 1; Length 368;
 Best Local Similarity 24.6%; Pred. No. 1;
 Matches 57; Conservative 37; Mismatches 101; Indels 37; Gaps 8;
 QY 84 YLLAISFSLKPYQVALVLM-----GCCPGGTISNIFTFWVDGMDISMTTCTVYALG 139
 DB 34 FIVAMFVQLITGITLAFRYTSEASCAFAVVOHLVREVAAGREFMLHTATFVFLCI 93
 QY 140 MMPLCTVLTWMSLQONLTIPYONIGITLVCTIVARGVYNNVMPQSKILIKIGAV 199
 DB 94 LHMTRGLYVMSYSY---LTTAMMS--GLVLYLTLLTATLAFGV--LPMQMS---FWGAT 144
 QY 200 VGVLLLVAVAGVLAAGKSWNSDITL---LTISFTPLIGHVTGLALFTHQSORCR 256
 DB 145 VITNLSPILPYLVPWMLGYYVSDVTLKRFVHLFLPGICIIIVLHFIYHLN----- 199
 QY 257 TISLETGAONIQMCTMLQLSF-----TAHLVQMLSPPLAYGLFOL 298
 DB 200 -----GSSNPAGIDTALKVAFPHMLMTDAKCLSYLIGLIFLQAAGFLMEL 245
 RESULT 15
 Y944 SYNY3 STANDARD; PRT; 383 AA.
 AC P74311;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein slr0944.
 GN SLR0944.
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 CX NCBI_Taxid=1148;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905221;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Saeemoto S., Kimura T.,
 RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-116(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE ACB3 FAMILY.
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 DR EMBL; D90914; BAA18405.1; -;
 DR InterPro; IPR004706; Acb3.
 DR Pfam; PF01758; SSB; 1.
 DR TIGRfam; TIGR00832; acb3; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 139 159 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 200 220 POTENTIAL.
 FT TRANSMEM 238 258 POTENTIAL.
 FT TRANSMEM 272 292 POTENTIAL.
 FT TRANSMEM 309 329 POTENTIAL.
 FT TRANSMEM 332 352 POTENTIAL.
 SQ SEQUENCE 383 AA; 42402 MW; 3D8C4CFB8A2F08B CRC64;
 Query Match 5.5%; Score 109.5; DB 1; Length 383;
 Best Local Similarity 20.9%; Pred. No. 1.6; Indels 49; Gaps 13;
 Matches 58; Conservative 55; Mismatches 115; Indels 49; Gaps 13;
 QY 40 VMGGLMPSLGSVEIRKLWSHIRPQGIAGVLLCOFGIMPTAYLLA---ISFLKPVQ 96
 DB 62 ICLFPMWYPIWVKIPFQSQARQAVKAPKPVILTVVNWIKPFTWYIFAGFFGLYFAPLL 121
 QY 97 AIAVILMGCCPGGTISNIF-----TFVVDGMDISMTTCTVYALGM 140
 DB 122 TATEIIRG--QEVTLANSYIAGCILLGAPCTAWVLM--GLYSYNOGLTVWVAVNSL 177
 QY 141 MPCLCTVLTWMSL---QONLTIPYONIGIT-LVCLTIPVAFGVYVY-----RW-PKQ 189
 DB 178 ANLFLYAPLPGKVLAAASNLTVWQIVLSVLIVGLPLAAGISYRWILKHKGRMPESQ 237
 QY 190 SKIILIGAVGVLLLV--AVAGVLAAGKSWNSDITLTI-----SFTPLIGHVTG 241
 DB 238 FLHYSLPIALVALLLTLLLFKGLKELVNNPLH--IFLIAVPLFIQNNFI-LITYVLG 294
 QY 242 FLIALFTHQSNORCTISLETGAONIQMCTMLQLSF 278
 DB 295 LKLKL-----SYDDAAPALIGASNHFEVALATVAVLF 327
 Search completed: June 9, 2003, 07:08:36
 Job time : 19 secs